

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: WAHL, DR, GEOFFREY M
O'GORMAN DR, STEPHEN V
- (ii) TITLE OF INVENTION: FLP-MEDIATED GENE MODIFICATION IN
MAMMALIAN CELLS, AND COMPOSITIONS AND CELLS USEFUL
THEREFOR
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: FITCH, EVEN, TABIN & FLANNERY
 - (B) STREET: 135 South LaSalle Street, Suite 900
 - (C) CITY: Chicago
 - (D) STATE: Illinois
 - (E) COUNTRY: USA
 - (F) ZIP: 60603
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/666,252
 - (B) FILING DATE: 08-MAR-1991
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: REITER MR, STEPHEN E
 - (B) REGISTRATION NUMBER: 31192
 - (C) REFERENCE/DOCKET NUMBER: 50730
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (619) 552-1311
 - (B) TELEFAX: (619) 552-0093
 - (C) TELEX: 20 6566 PATLAW CGO

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

(B) CLONE: NATIVE FLP

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG CCA CAA TTT GAT ATA TTA TGT AAA ACA	CCA CCT AAG GTG CTT GTT	48
Met Pro Gln Phe Asp Ile Leu Cys Lys Thr	Pro Pro Lys Val Leu Val	
1 5 10 15		
CGT CAG TTT GTG GAA AGG TTT GAA AGA CCT	TCA GGT GAG AAA ATA GCA	96
Arg Gln Phe Val Glu Arg Phe Glu Arg Pro	Ser Gly Glu Lys Ile Ala	
20 25 30		
TTA TGT GCT GCT GAA CTA ACC TAT TTA TGT	TGG ATG ATT ACA CAT AAC	144
Leu Cys Ala Ala Glu Leu Thr Tyr Leu Cys	Trp Met Ile Thr His Asn	
35 40 45		
GGA ACA GCA ATC AAG AGA GCC ACA TTC ATG	AGC TAT AAT ACT ATC ATA	192
Gly Thr Ala Ile Lys Arg Ala Thr Phe Met	Ser Tyr Asn Thr Ile Ile	
50 55 60		
AGC AAT TCG CTG AGT TTC GAT ATT GTC AAT	AAA TCA CTC CAG TTT AAA	240
Ser Asn Ser Leu Ser Phe Asp Ile Val Asn	Lys Ser Leu Gln Phe Lys	
65 70 75 80		
TAC AAG ACG CAA AAA GCA ACA ATT CTG GAA	GCC TCA TTA AAG AAA TTG	288
Tyr Lys Thr Gln Lys Ala Thr Ile Leu Glu	Ala Ser Leu Lys Lys Leu	
85 90 95		
ATT CCT GCT TGG GAA TTT ACA ATT ATT CCT	TAC TAT GGA CAA AAA CAT	336
Ile Pro Ala Trp Glu Phe Thr Ile Ile Pro	Tyr Tyr Gly Gln Lys His	
100 105 110		

CAA TCT GAT ATC ACT GAT ATT GTA AGT AGT TTG CAA TTA CAG TTC GAA Gln Ser Asp Ile Thr Asp Ile Val Ser Ser Leu Gln Leu Gln Phe Glu 115 120 125	384
TCA TCG GAA GAA GCA GAT AAG GGA AAT AGC CAC AGT AAA AAA ATG CTT Ser Ser Glu Glu Ala Asp Lys Gly Asn Ser His Ser Lys Lys Met Leu 130 135 140	432
AAA GCA CTT CTA AGT GAG GGT GAA AGC ATC TGG GAG ATC ACT GAG AAA Lys Ala Leu Leu Ser Glu Gly Glu Ser Ile Trp Glu Ile Thr Glu Lys 145 150 155 160	480
ATA CTA AAT TCG TTT GAG TAT ACT TCG AGA TTT ACA AAA ACA AAA ACT Ile Leu Asn Ser Phe Glu Tyr Thr Ser Arg Phe Thr Lys Thr Lys Thr 165 170 175	528
TTA TAC CAA TTC CTC TTC CTA GCT ACT TTC ATC AAT TGT GGA AGA TTC Leu Tyr Gln Phe Leu Phe Leu Ala Thr Phe Ile Asn Cys Gly Arg Phe 180 185 190	576
AGC GAT ATT AAG AAC GTT GAT CCG AAA TCA TTT AAA TTA GTC CAA AAT Ser Asp Ile Lys Asn Val Asp Pro Lys Ser Phe Lys Leu Val Gln Asn 195 200 205	624
AAG TAT CTG GGA GTA ATA ATC CAG TGT TTA GTG ACA GAG ACA AAG ACA Lys Tyr Leu Gly Val Ile Ile Gln Cys Leu Val Thr Glu Thr Lys Thr 210 215 220	672
AGC GTT AGT AGG CAC ATA TAC TTC TTT AGC GCA AGG GGT AGG ATC GAT Ser Val Ser Arg His Ile Tyr Phe Phe Ser Ala Arg Gly Arg Ile Asp 225 230 235 240	720
CCA CTT GTA TAT TTG GAT GAA TTT TTG AGG AAT TCT GAA CCA GTC CTA Pro Leu Val Tyr Leu Asp Glu Phe Leu Arg Asn Ser Glu Pro Val Leu 245 250 255	768
AAA CGA GTA AAT AGG ACC GGC AAT TCT TCA AGC AAT AAA CAG GAA TAC Lys Arg Val Asn Arg Thr Gly Asn Ser Ser Ser Asn Lys Gln Glu Tyr 260 265 270	816
CAA TTA TTA AAA GAT AAC TTA GTC AGA TCG TAC AAT AAA GCT TTG AAG Gln Leu Leu Lys Asp Asn Leu Val Arg Ser Tyr Asn Lys Ala Leu Lys 275 280 285	864
AAA AAT GCG CCT TAT TCA ATC TTT GCT ATA AAA AAT GGC CCA AAA TCT Lys Asn Ala Pro Tyr Ser Ile Phe Ala Ile Lys Asn Gly Pro Lys Ser 290 295 300	912

CAC ATT GGA AGA CAT TTG ATG ACC TCA TTT CTT TCA ATG AAG GGC CTA 960
 His Ile Gly Arg His Leu Met Thr Ser Phe Leu Ser Met Lys Gly Leu
 305 310 315 320

 ACG GAG TTG ACT AAT GTT GTG GGA AAT TGG AGC GAT AAG CGT GCT TCT 1008
 Thr Glu Leu Thr Asn Val Val Gly Asn Trp Ser Asp Lys Arg Ala Ser
 325 330 335

 GCC GTG GCC AGG ACA ACG TAT ACT CAT CAG ATA ACA GCA ATA CCT GAT 1056
 Ala Val Ala Arg Thr Thr Tyr Thr His Gln Ile Thr Ala Ile Pro Asp
 340 345 350

 CAC TAC TTC GCA CTA GTT TCT CGG TAC TAT GCA TAT GAT CCA ATA TCA 1104
 His Tyr Phe Ala Leu Val Ser Arg Tyr Tyr Ala Tyr Asp Pro Ile Ser
 355 360 365

 AAG GAA ATG ATA GCA TTG AAG GAT GAG ACT AAT CCA ATT GAG GAG TGG 1152
 Lys Glu Met Ile Ala Leu Lys Asp Glu Thr Asn Pro Ile Glu Glu Trp
 370 375 380

 CAG CAT ATA GAA CAG CTA AAG GGT AGT GCT GAA GGA AGC ATA CGA TAC 1200
 Gln His Ile Glu Gln Leu Lys Gly Ser Ala Glu Gly Ser Ile Arg Tyr
 385 390 395 400

 CCC GCA TGG AAT GGG ATA ATA TCA CAG GAG GTA CTA GAC TAC CTT TCA 1248
 Pro Ala Trp Asn Gly Ile Ile Ser Gln Glu Val Leu Asp Tyr Leu Ser
 405 410 415

 TCC TAC ATA AAT AGA CGC ATA TAAGTACGCA TTAAAGCATA AACACGCACT 1299
 Ser Tyr Ile Asn Arg Arg Ile
 420

 ATGCCGTTCT TCTCATGTAT ATATATATAC AGGCAACACG CAGATATAGG TGCGACGTGA 1359
 ACAGTGAGCT GTATGTGCGC A 1380

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Pro	Gln	Phe	Asp	Ile	Leu	Cys	Lys	Thr	Pro	Pro	Lys	Val	Leu	Val	1	5	10	15
Arg	Gln	Phe	Val	Glu	Arg	Phe	Glu	Arg	Pro	Ser	Gly	Glu	Lys	Ile	Ala	20	25	30	
Leu	Cys	Ala	Ala	Glu	Leu	Thr	Tyr	Leu	Cys	Trp	Met	Ile	Thr	His	Asn	35	40	45	
Gly	Thr	Ala	Ile	Lys	Arg	Ala	Thr	Phe	Met	Ser	Tyr	Asn	Thr	Ile	Ile	50	55	60	
Ser	Asn	Ser	Leu	Ser	Phe	Asp	Ile	Val	Asn	Lys	Ser	Leu	Gln	Phe	Lys	65	70	75	80
Tyr	Lys	Thr	Gln	Lys	Ala	Thr	Ile	Leu	Glu	Ala	Ser	Leu	Lys	Lys	Leu	85	90	95	
Ile	Pro	Ala	Trp	Glu	Phe	Thr	Ile	Ile	Pro	Tyr	Tyr	Gly	Gln	Lys	His	100	105	110	
Gln	Ser	Asp	Ile	Thr	Asp	Ile	Val	Ser	Ser	Leu	Gln	Leu	Gln	Phe	Glu	115	120	125	
Ser	Ser	Glu	Glu	Ala	Asp	Lys	Gly	Asn	Ser	His	Ser	Lys	Lys	Met	Leu	130	135	140	
Lys	Ala	Leu	Leu	Ser	Glu	Gly	Glu	Ser	Ile	Trp	Glu	Ile	Thr	Glu	Lys	145	150	155	160
Ile	Leu	Asn	Ser	Phe	Glu	Tyr	Thr	Ser	Arg	Phe	Thr	Lys	Thr	Lys	Thr	165	170	175	
Leu	Tyr	Gln	Phe	Leu	Phe	Leu	Ala	Thr	Phe	Ile	Asn	Cys	Gly	Arg	Phe	180	185	190	
Ser	Asp	Ile	Lys	Asn	Val	Asp	Pro	Lys	Ser	Phe	Lys	Leu	Val	Gln	Asn	195	200	205	
Lys	Tyr	Leu	Gly	Val	Ile	Ile	Gln	Cys	Leu	Val	Thr	Glu	Thr	Lys	Thr	210	215	220	
Ser	Val	Ser	Arg	His	Ile	Tyr	Phe	Phe	Ser	Ala	Arg	Gly	Arg	Ile	Asp	225	230	235	240
Pro	Leu	Val	Tyr	Leu	Asp	Glu	Phe	Leu	Arg	Asn	Ser	Glu	Pro	Val	Leu	245	250	255	

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Lys	Arg	Val	Asn	Arg	Thr	Gly	Asn	Ser	Ser	Asn	Lys	Gln	Glu	Tyr	
260						265						270			
Gln	Leu	Leu	Lys	Asp	Asn	Leu	Val	Arg	Ser	Tyr	Asn	Lys	Ala	Leu	Lys
275						280						285			
Lys	Asn	Ala	Pro	Tyr	Ser	Ile	Phe	Ala	Ile	Lys	Asn	Gly	Pro	Lys	Ser
290						295						300			
His	Ile	Gly	Arg	His	Leu	Met	Thr	Ser	Phe	Leu	Ser	Met	Lys	Gly	Leu
305				310						315			320		
Thr	Glu	Leu	Thr	Asn	Val	Val	Gly	Asn	Trp	Ser	Asp	Lys	Arg	Ala	Ser
			325						330			335			
Ala	Val	Ala	Arg	Thr	Thr	Tyr	Thr	His	Gln	Ile	Thr	Ala	Ile	Pro	Asp
			340			345						350			
His	Tyr	Phe	Ala	Leu	Val	Ser	Arg	Tyr	Tyr	Ala	Tyr	Asp	Pro	Ile	Ser
355						360						365			
Lys	Glu	Met	Ile	Ala	Leu	Lys	Asp	Glu	Thr	Asn	Pro	Ile	Glu	Glu	Trp
370						375						380			
Gln	His	Ile	Glu	Gln	Leu	Lys	Gly	Ser	Ala	Glu	Gly	Ser	Ile	Arg	Tyr
385				390						395			400		
Pro	Ala	Trp	Asn	Gly	Ile	Ile	Ser	Gln	Glu	Val	Leu	Asp	Tyr	Leu	Ser
			405						410			415			
Ser	Tyr	Ile	Asn	Arg	Arg	Ile									
			420												